

Table S4 *TGFBR2*, *CCND1* and *STAT3* SNPs associated with overall breast cancer risk stratified by ER status.

SNP	Chr.	Position	Gene	Minor allele	MAF	ER-positive breast cancer		ER-negative breast cancer		Case-only analysis (ER+ vs ER-)	
						OR ^a (95%CI)	p-value	OR ^a (95%CI)	p-value	p -value	
rs1431131	3	30675880	<i>TGFBR2</i>	A	0.36	1.06 (1.04-1.09)	2.7×10 ⁻⁷	1.01 (0.97-1.05)	0.61	0.01	
rs1192442	3	30677484	<i>TGFBR2</i>	C	0.41	0.94 (0.92-0.97)	1.2×10 ⁻⁶	0.99 (0.95-1.03)	0.69	0.02	
rs7177	11	69466115	<i>CCND1</i>	C	0.47	0.95 (0.93-0.97)	8.2×10 ⁻⁶	0.99 (0.95-1.03)	0.61	0.04	
rs1905339	17	40582296	<i>STAT3</i>	G	0.33	1.05 (1.03-1.08)	5.3×10 ⁻⁵	1.04 (1.00-1.08)	0.07	0.62	

^a OR adjusted for age, study and nine European principal components.

ER, estrogen receptor; SNP, single nucleotide polymorphism; Chr., chromosome; MAF, minor allele frequency; OR, odds ratio; CI, confidence interval; *TGFBR2*, transforming growth factor beta receptor II; *CCND1*, cyclin D1; *STAT3*, signal transducer and activator of transcription 3.